Page 2

Table II. C-1027 gene cluster open reading frames (27 to 42), primers for ORF amplification, and

proposed functions

ORF	Relative	Primers Functio	n SEQ
	Position		ID
			NO.
orf-	43945-46023	Fwd: GTG TGC CCG GTG ACA GAC Antibio	tic 71
27		Rev: TCA GCC CAC GGG CTG GGA Transpo	rter 72
orf-	46167-47171	Fwd: GTG TTG GGC GAT GAG GAC O-	73
28		Rev: TCA GAC CGC GGA CAT CTG methylt ase	ransfer 74
orf	47227-48485	Fwd: ATG GCC GGC CTG GTC ATG p450	75
29		Rev: TCA GGA CCC GAG GGT CAC hydroxy	lase 76
orf-	48610-49714	Fwd: GTG GAC CAG ACG TCT ACG Oxidore	ductase 77
30		Rev: TCA TGC AGG TGC AGC GTG	78
orf-	50350-51390	Fwd: ATG AGG CCG CTC GTT CGG Unknown	
31		Rev: TCA TCC CGG CCC GGC GGC Protein	80
orf-	51420-52341	Fwd: ATG AGA ACG CGG CGA CGC Oxidore	ductase 81
32		Rev: TCA CGG CCG GAG GCG TAC	82
orf-	53241-54074	Fwd: GTG TAT CAG CCG GAC TGT Unknown	83
33		Rev: CTA CTC ATT CCA GTT GTG Protein	84
orf-	54230-55379	Fwd: ATG TCT ACG GGC TAT CTC Unknown	85
34		Rev: TCA GCC GCC GGT GGC GCC Protein	86
orf-	56027-56881	Fwd: ATG TTC TCC CCC GCC GCC Oxidase	•
35		Rev: TCA GTA CGC CTG GTG GGC Dehydro	genase 88
orf-	56928-57730	Fwd: ATG AAT TCG CTC GAC GAC Unknown	
36		Rev : TCA GCT CCC GGT CGC CGC Protein	90
orf-	57834-58304	Fwd: ATG ACC GCG ACG AAT CCT Regulat	
37		Rev: CTA GGC GGC GCG TCC CGC	92
orf-	58440-60091	Fwd: ATG AGC ACC ACG GCC GAG Oxidore	
38		Rev: TCA GCC GCG CGC CGA CGG	94
orf-	60092-60622	Fwd: ATG ACC CTG GAG GCC TAC Regulat	
39		Rev: TCA TGC GGG GCT CCC GGT	96
orf-	60940-62020	Fwd: GTG AAA AGT GAC TCT GCC Regulat	_
40		Rev: TCA ACG GCG AGT TGG CTG	98
orf-	62045-62899	Fwd: GTG ACC ACG AAC ACC ATC Regulat	-
41		Rev: TCA CCC GCG ATC TCG ATC	100
orf-	62788-63164	Fwd: (partial ORF) p450	101
42		Rev: TCA CCT CGC CGT ACT CAC hydroxy	lase [10 :

Delete the paragraphs at page 41, lines 3-25 and insert the following:

For type II PKS, the following two pairs of degenerate primers were used—5'-AGC TCC ATC AAG TCS ATG RTC GG-3' (forward, SEQ ID NO:102[103]) / 5'-CC GGT GTT SAC SGC GTA GAA CCA GGC G-3' (reverse, SEQ ID NO:103[104]) and 5'-GAC ACV GCN TGY TCB





Application No.: 09/478,188

Page 3

TCV-3' (forward, SEQ ID NO:104[105])/5'-RTG SGC RTT VGT NCC RCT-3' (SEQ ID NO:105[106]) (B, C+G+T; N, A+C+G+T; R, A+G; S, C+G; V, A+C+G; Y, C+T) (reverse) (Seow *et al.* (1997) *J. Bacteriol.*, 179: 7360-7368). No product was amplified under all conditions tested. For type I PKS, the following pair of degenerate primers were used—5'-GCS TCC CGS GAC CTG GGC TTC GAC TC-3' (forward, SEQ ID NO:106[107]) / 5'-AG SGA SGA SGA GCA GGC GGT STC SAC-3' (S, G+C) (reverse, SEQ ID NO:107[108]) (Kakavas *et al.* (1997) *J. Bacteriol.*, 179: 7515-7522). A distinctive product with the predicted size of 0.75 kb was amplified in the presence of 20% glycerol and cloned into pGEM-T according to the protocol provided by the manufacturer (Promega) to yield pBS1001.

For NGDH, the following pair of degenerate primers were used—5'-CS GGS GSS GCS GGS TTC ATC GG-3' (forward, SEQ ID NO: 108[109]) / 5'-GG GWR CTG GYR SGG SCC GTA GTT G-3' (R, A+G; S, C+G; W, A+T; Y, C+T) (reverse, SEQ ID NO: 109[110]) (Decker, et al. (1996) FEMS Lett., 141: 195-201). A distinctive product with the predicted size of 0.55 kb was amplified and cloned into pGEM-T to yield pBS1002.

For *cagA*, the following pair of primers, flanking its coding region, were used—5'-AG GTG GAG GCG CTC ACC GAG-3' (forward, SEQ ID NO:<u>110</u>[111])/5'-G GGC GTC AGG CCG TAA GAA G-3' (reverse, SEQ ID NO:<u>111</u>[112]) (Sakata *et al.* (1992) *Biosci. Biotechnol. Biochem., 56: 159201595). A distinctive product with the predicted size of 0.73 kb was amplified from pBS1005 and cloned into pGEM-T to yield pBS1003.*

Delete the paragraphs at page 14, lines 11-22 and insert the following:

Figure 6 shows the DNA (SEQ ID NO:112) and deduced amino acid sequences of the 3.0-kb BamHI fragment from pBS1007, showing the sgcA (SEQ ID NO:113) and sgcB genes (SEQ ID NO:114). Possible RBSs are boxed. The presumed translational start and stop sites are in boldface. Restriction enzyme sites of interest are underlined. The amino acids, according to which the degenerated PCR primer were designed for amplifying the dNDP-glucose 4,6-dehydratase gene from S. globisporus, are underlined.

Figure Shows the amino acid sequence alignment of SgcA (SEQ ID NO:113) with three other dNDP-glucose 4,6-dehydratases. Gdh, TDP-glucose 4,6-dehydratase of *S. erythraea* (AAA68211) (SEQ ID NO:115); MtmE, TDP-glucose 4,6-dehydratase in the mithramycin pathway of *S. argillaceus* (CAA71847) (SEQ ID NO:117); TylA2, TDP-glucose 4,6-dehydratase in the tylosin

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2